SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SAMSON, MICHEL PARMENTIER, MARC VASSART, GILBERT LIBERT, FREDERICK
- (ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
- (iii) NUMBER OF SEQUENCES: 17
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE\ Knobbe, Martens, Olson & Bear
 - (B) STREET: 620 Newport Center Drive 16th Floor
 - (C) CITY: Newport Beach
- (D) STATE: CA
- 山 (E) COUNTRY: U.S.A.
- ΠJ
- (IV) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Rloppy disk
 - (B) COMPUTER: IBM &C compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Paten In Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER \ 08/833,752
 - (B) FILING DATE: 9-APR-1997
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Altman, Daniel E
 - (B) REGISTRATION NUMBER: 34, 15
 - (C) REFERENCE/DOCKET NUMBER:
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 240..791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AATG GAT TAT CAA GTG TCA AGT CCA AGT CTTTTTATT ATGCACAGGG TAGARCAAG 287 ATG GAT TAT CAA GTG TCA AGT CCA AGT CCA ATC TAT GAC AGT CAAT TAT TAT ACA 287 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr 1	GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAGCTAG CAGCAAACCT TCCCTTCACT ACAAAACTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCATTCATG GAGGGCAACT	60 120 180
ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC TAT TAT GAC ATC TAT TAT GAC ATC TAT TAT ACA CATC TAT TAT GAC AST TAT TAT ACA CATC TAT TAT GAC AST TAT TAT TAT ACA CATC TAT TAT GAC AST TAT TAT TAT TAT TAT TAT TAT TAT TAT	ANATHORNER TAGGACTETA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG	
Met	AND CAN TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA	287
TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CTC Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu 20 CTG CTC CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC ATC Leu Dro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn ATG Leu GTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG ATG Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met ATG Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met ATG Leu CTG ATC CTC AAC CTG GCC AAC CTG GCC ATC TCT GAC CTG AAG AGC ATG ATC TAC TAC CTC AAC CTG AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT ATT LATT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC GCC CAG TGG GAC TTT CTT LACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC GCC CAG TGG GAC TTT ACT TGT CAC ATC TTC ATC CTG GCC CAC TAT GCT GCC GCC CAG TGG GAC TTT CTT LACT GTC CCC TTC TGG GCT CAC TTT AAA AAC TGC GCC GCC CAG TGG GAC TTT ACT GTC CCC TTC TTC ATC ATC TTG ACA GGG CTC TAT TTT ATA GGC TTC GGA AAAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC GGA AAAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC TTC ACC TGC GTC CAT GCT GTG ATC TTC TGT ACA ATC GAT AGG TAC TTC ALE VAL VAL HIS ALS VAL PHE ALS LEU LEU THY ILE ASP ARG TAC CTG ALS VAL VAL HIS ALS ALS VAL PHE ALS LEU LYS ALS ARG TTC TTC ACC TTT ALS VAL VAL VAL HIS ALS ALS VAL PHE ALS LEU LYS ALS ARG TTC TTC ACC TTT ALS VAL VAL VAL HIS ALS ALS VAL PHE ALS LEU LYS ALS ARG TTC TTC ACC TTT ALS VAL VAL VAL HIS ALS ALS VAL PHE ALS LEU LYS ALS ARG TTC TTC ACC TTC ACC TGC AGC TC ACT ATT ACC AGA TCT CAA AAC AGG CTC TTC TAC TAC TCT CCA GGA ATC ACT TTT ACC AGA TCT CAA AAC AGG CTC TTC TAC ACC TGC AGC TCT CAT TTT CCA TAC ATC CAA AAC AGG CTC CAT TAC TCT CCA AGC TCT CAT TTT CCA TAC ATC CAA AAC AGG TCT CAT TAC TCT CCA AGC TCT CAT TTT CCA TAC ATC TTC CAA AAC AGG TCT CAT TAC TCT CCA AGC TCT CAT TTT CCA TAC ATC TTC TAC TAC TCT CCA AGC TCT CAT TTT CCA TAC ATC TTC CAA AAC AGG TCT CAT TAC TCT CCA AGC TCT CAT TTT CCA TAC TCC TAC TAC TAC TCT CCA AGC TCT CAT	Mot Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr	
TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC Ser Glu Pro Cys Glu Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu 20 20 25 25 25 25 25 25 25 25 25 25 25 25 25	- 10 IS	
Ser Glu	TOO ONG COC TOO CAN AND ATC ANT GTG ANG CAN ATC GCA GCC CGC CTC	335
CTG CTC CCG CTC TAC CTC	TCG GAG CCC TGC CAA AAA ATC MIT GTG TAIS GTD TTE Ala Ala Arg Leu	
CTG CCG CTC CCG CTC CTC CTC CTC CTG CTG CTC CTG		
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Ash 45 and 4		383
ATG CTG GTC ATC CTC ATC CTG ATC CTG AAC AGC CTG AAG AGC ATG Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	THE TET CCG CTC TAC TCA CTG GTG TTC ATC TTT GGV Phe Val Glv Asn	•
ATG TG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met 1		
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met		431
ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT ATC CTT Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu 65° 70° 80° 70° 70° 70° 70° 70° 70° 70° 70° 70° 7	ATG FETG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG LVG ATG LVG Ser Met	
ACT FAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT Thrulasp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu 80 65 80 70 80 80 80 80 80 80 80 80 80 80 80 80 80		•
Act SAC Arc Tac Cro Cro Arc Tac Cro Arc		479
CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT 527 Leuthr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe 85 90 95 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC 575 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe 11e Gly Phe 110 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG ASP Arg Tyr Leu 120 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT AAA AAA GCC AGG ACG GTC ACC TTT AAA AAA GCC AGG ACG GTC ACC TTT AAA AAA AAA AAA AAA AAA AAA A	ACTIGAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC GTT	
CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT Leuwthr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe 85 GAAAT ACA ATG TGT CAC AGA CTC TTG ACA GGG CTC TAT TTT ATA GGC TCC GGY AND TAT TTC TCT GGA ATC TTC TCT GGA ATC TTC TTC ATC ATC ATC TTT GCG TAT TTT ILeuwthr Indicate Indin		
Leuthr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe 85 GGA MAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 100 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 115 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 GGG GTG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GTG TTT GCG TCT Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC 160 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	669 /U /3 ·	527
GGA FAAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC Gly FASN Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 100 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG ACA ATC GAT ACA ATC ACA ATC GAT ACA ACA ACA ATC GAT ACA ACA ACA ACA ACA ACA ACA ACA ACA A	CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG 199 GAC 111	<i>327</i> ,
GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC 575 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 100 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG ACA ATC GAT ACA ATC GAT AGG TAC CTG ACA ATC GAT ACA ACA ATC GAT ACA ACA ACA ACA ACA ACA ACA ACA ACA A		
GIATAT ACA ATG IGT CAA CIC TIG AGG GOO CIC TATA CIC TIG GIY Leu Tyr Phe Ile Gly Phe 100 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG 623 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 125 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT 671 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GTG GTT GCT TTT GCG TCT 719 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 150 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC 767 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A 792 Thr Cys Ser Ser His Phe Pro Tyr	n: 70	575
TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 115 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	GGA FAAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT III AIA GGC IIC	5/5
TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 115 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe 11e Gly Phe	
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 125 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT 671 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT 719 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 150 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC 767 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A 792 Thr Cys Ser Ser His Phe Pro Tyr	100 105	(22
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 125 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT 671 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT 719 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 150 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC 767 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A 792 Thr Cys Ser Ser His Phe Pro Tyr	TTC TCT GGA ATC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG	623
GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val III Phe 130 135 140 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GTG GTG TTT GCG TCT Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 150 155 160 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	115 120 125	C71
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val III Phe 130 135 140 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GTG GTG TTT GCG TCT Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 150 155 160 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT	P/T
GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GTG GTG TTT GCG TCT Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val The	
GGG GTG GTG ACA AGI GTG ATC ACI TGG GTG GTG GTG GTG ACA AGI GTG ATC ACI TGG GTG GTG GTG ACA AGI GTG ATC ACI TGG GTG GTG GTG ACA AGI GTG ATC ACI TGG GTG GTG GTG GTG ACA AGI GTG GTG GTG GTG GTG ACC TCT CAT TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC TGG GTG GTG AGC TCT CAT TAC ACC TGC AGC TCT CAT TTT CCA TAC A	136 140	==0
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GTG TTT GCG TCT	719
145 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser	
CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	145 150 155 160	
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu HIS Tyr 165 170 175 ACC TGC AGC TCT CAT TTT CCA TAC A 792 Thr Cys Ser Ser His Phe Pro Tyr	CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC	767
ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr 792	Leu Pro Gly lle lle Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr	
ACC TGC AGC TCT CAT TTT CCA TAC A Thr Cys Ser Ser His Phe Pro Tyr	165 170 175	
Thr Cys Ser Ser His Phe Pro Tyr		792
	Thr Cvs Ser Ser His Phe Pro Tyr	
100	180	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 240..1295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAGCTAG CAGCAAACCT	60
TO COUNTRY OF A CARARACTE ATTICCTTCCC CARARAGAGA GITARITUAL IGIAGACAIC	120
TANACCOA ATTANANACO TATTCATCTA TAAAACAGTT TGCATTCATG GAGGGCAACT	180
AND TO THE CAMPO THE CONCERT AND ADACATCA CTTTTTATT AT GCACAGG I GGAACAAG	239
ANG TONE ON COLORED TO ACT COL ATC TAT GAC ATC AAT TAT TAT ACA	287
Met Asp Tyr Gln Val Ser Ser Pro 11e Tyr Asp 11e Ash 191 191 1111	
TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC	335
Ser Clu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu	
CTG CCT CCC CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC	383
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn 45	
ATGUETG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG	431
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	
≘ sn 55	
ACTIONS ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT.	479
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu	
6E 70 /5	
COTT ACT COTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT	527
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe	
90	
GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC	575
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe 11e Gly Fhe	
100 105	603
THE TET CEN ATE THE ATE ATE ATE CTE CTE ACA ATE GAT AGG TAC CTE	623
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	
115 120	C71
GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT	671
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe	•
120 135 I4U	710
COC OTC CTC ACA ACT CTC ATC ACT TGG GTG GTG GTG TTT GCG TCT	719
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val File Ala Ser	
145 150 155	767
CTC CCA CCA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CII CAI TAC	/6/
Ley Pro Gly Tie Tie Phe Thr Ard Ser Gin Lys Glu Gly Leu His Tyl	
165 170 175	

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ACC	TGC	AGC	TCT	CAT	TTT	CCA	TAC	AGT	CAG	TAT	CAA	TTC	TGG	AAG	AAT	013
Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Pne	пр	гÀг	ASII	
			100					185					130			062
TTC	CAG	ACA	TTA	AAG	ATA	GTC	ATC	TTG	GGG	CTG	GTC	CTG	CCG	CTG	CFT	863
Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu	
							200					203				911
GTC	ATG	GTC	ATC	TGC	TAC	TCG	GGA	ATC	CTA	AAA	ACT	CTG	CTT	CGG	TGT	ATT
Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	IIII	Tea	Leu	Arg	Cys	
						21 5					220			_		959
CGA		GAG	AAG	AAG	AGG	CAC	AGG	GCT	GTG	AGG	CTT	ATC	TTC	ACC	ATC	959
Ara	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	IIe	Pne	Thr	110	
					ววก					2.30					240	1007
	ATT	GTT	TAT	TTT	CTC	TTC	TGG	GCT	CCC	TAC	AAC	ATT	GTC	CTT	CrC	1007
Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	Asn	He	vai	ne u	цси	•
				215					250					233		1055
CTG	AAC	ACC	TTC	CAG	GAA	TTC	TTT	GGC	CTG	AAT	TAA	TGC	AGT	AGC	TCT	1055
Leu	=Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Jer	Ser	Ser	
			$\sim \sim \sim$					ノカラ					2,0			1102
AAC	₩ AGG	TTG	GAC	CAA	GCT	ATG	CAG	GTG	ACA	GAG	ACT	CTT	GGG	ATG	ACG	1103
Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	пеи	GTA	Met	Tnr ,	
	ليتية	~ ~ ~					- 2×0					200				11F1
CAC	HGC	maa	ATC	AAC	CCC	ATC	ATC	TAT	GCC	TTT	GTC	GGG	GAG	AAG	TTC	1151
His	Cvs	Cvs	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	vai	GIY	GIu	ьуs	Pne	
	11600					295					300					1100
AGA	\mathbf{m}	TAC	CTC	TTA	GTC	TTC	TTC	CAA	AAG	CAC	ATT	GCC	AAA	CGC	TTC	1199
Arg	≛ Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	HIS	Ile	Ala	гàг	Arg	FILE	
205	 -				วาก					310					320	1247
	A	TGC	TGT	TCT	ATT	TTC	CAG	CAA	GAG	GCT	CCC	GAG	CGA	GCA	AGC	124/
Cvs	Lvs	Cvs	Cys	Ser	Ile	Phe	Gln	Gln	GIu	Alạ	Pro	GIu	Arg	Ala	ser	
	==			つつに					330					222		1205
TCA	GTT	TAC	ACC	CGA	TCC	ACT	GGG	GAG	CAG	GAA	ATA	TCT	GIG	GGC	TTG	1295
Ser	Wal	Tyr	Thr	Arg	Ser	Thr	Gly	Glu	Gln	Glu	Ile	Ser	vai	GIŻ	Leu	
	-		240	•				345					220			1255
TGA	CACG	GAC	TCAA	GTGG	GC T	GGTG	ACCC	A GT	CAGA	GTTG	TGC	ACAT	GGC	TTAG	TTTTCA	1355
		~~~	~~~~	maaa	$\alpha \alpha - \alpha$	እየርርጥ	$\mathbf{TCCNI}$	N (2A	(3(3,1,0)	4"1"1"1	LIA	HANG	Gran .	GIIL	CIGILL	1415
TAG	AGGG	TCT	AAGA	TTCA	TC C	ATTT	TTTA	G GC	ATCT	GTTT	AAA	GTAG	ATT .	AGA'I'	CCGAAT	1475
TC														_		1477

### (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - $(\tilde{A})$  LENGTH: 1442 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS

### (B) LOCATION: 240..884

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

	<b>\</b>	_	•														
CAAT	ייירר	CC A	ACAG	AGCC	A AC	CTCI	CCAT	CTA	GTGG	ACA	GGGA	AGCI	'AG C	'AGCA	AACCT		. 60
maaa		מ ידור	ת ת תים	רידים מ	רכ איז	ጉጉርጥ	ጕርርር	: CAA	AAAG	AGA	GTTP	$\Delta TTC$	AA I	GIAG	MCAIC		120
mama	3m 2 CC	ל מישי	ע עייים	אממג	יר דו	ኒጥጥር ጀ	$\mathbf{T}$	A TAP	<b>LAACA</b>	$\mathbf{GTT}$	TGCA	TTCP	ITG C	JOUA	CAACT		180
3335	n 2 (2 ) (1	יתיי ח	יאככא	الششا	מידי מיז	ΙΔΑΔΟ	PATCA	A CTT	TTTP	TTTT	ATGC	ACAC	1 DD	GGAP.	CAAG		239
3 000	CAT	ጥአጥ	ממכ	CTG	ፐሮል	AGT	CCA	ATC	TAT	GAC	ATC	AAT	TAI	IAI	ACA		287
AIG	GAI	TAL	Gln	Val	Ser	Ser	Pro	Ile	Tvr	Asp	Ile	Asn	Tyr	Tyr	Thr		
Mec	Asp	ıyı	GIII	5	502				10	~			•	15			
TOC	CAC	CCC	TGC	ממי	מממ	ATC	TAA	GTG	AAG	CAA	ATC	GCA	GCC [']	CGC	CTC		335
106	GAG	D~	CVC	Gln	LAZ	Ile	Asn	Val	Lvs	Gln	Ile	Ala	Ala	Arg	Leu .		
ser	GIU	PIO		GIII	цуз			25	1-		_		30	_	•		
ama	COM	000	20	ጥአሮ	ጥሮል	CTG	GTG	TTC	ATC	ттт	GGT	TTT	GTG	GGC	AAC		383
CIG	CCT	CCG	CIC	TAC	Cor	Leu	Val	Phe	Tle	Phe	Glv	Phe	Val	Gly	Asn		
ьeu	器o		пеп	IYI	Ser	пси	40	1 110			1	45		-			
	Ž.	35	N CC	CTC	አጥሮ	·CTG		ממכ	TGC	ΔΔΔ	AGG	CTG	AAG	AGC	ATG		431
ATG	CIG	GIC	AIC	CIC	TIO	Leu	Tla	yeu Zuic	Cve	Lvs	Arg	Leu	Lvs	Ser	Met		
Met		vaı	me	Leu	TIE	55	116	H311	Cys	<b>1</b> ,5	60		_,_		•	•	
	₩50		ma 0	OTH <b>C</b>	CTC.	AAC	СТС	CCC	አጥሮ	тст		CTG	TTT	TTC	CTT		479
ACT	GAC	ATC	TAC	CIG	CIC	Asn	LOU	פות	Tla	Ser	Asp	Leu	Phe	Phe	Leu		
		lle	Tyr	Leu	. Leu	ASII	пеп	AIA	116	75	11.55				80		
65	12			mm.c	70	GCT	CAC	ጥለጥ	CCT		GCC	CAG	TGG	GAC	TTT		527
CTT	ACT	GTC	CCC	TTC	TGG	Ala	Uic	TAI	λla	λla	Δla	Gln	Trp	Asp	Phe		
Leu	Thr	Val	Pro		Trp	Ala	HIS	ıyı	90	AIG	AIG	<u> </u>		95			•
	띹			85	<b>CD</b> N	OTE C	Tranco	א כי א		СТС	тат	ттт	АТА		TTC		575
GGA	TAAT	ACA	ATG	TGT	CAA	CTC	116	ACA Th~	Clv	Tou	ጥኒያ	Phe	Tle	Glv	Phe		• . •
Gly	Asn	Thr		Cys	GIn	Leu	ьeu	1111	GIY	neu,	TYL	1 110	110	0-1			
	Ŧ		100			3.00	3 m/C	105	CTC	א כי א	אתכ	САТ		TAC	CTG		623
TTC	<b>TCT</b>	GGA	ATC	TTC	TTC	ATC	AIC	CIC	CIG	Th~	Tlo	Agn	Ara	Tvr	Leu		
Phe	₽Ser		Ile	Phe	Pne	Ile	TTE	ьeu	Leu	TIII	116	125	mrg	-11-	200	•	
		115			~~~	mmm	120	mma	מממ	CCC	NGG		GTC	ACC	ጥጥጥ		671
GCT	GTC	GTC	CAT	GCT	GTG	TTT	GCT	IIA	AAA	712	AGG.	Thr	Val	Thr	Phe		• • •
Ala	Val	Val	His	Ala	Val	Pne	Ala	Leu	ьys	Ala	140	1111	Val	1111	Phe		
•	130					135	3 Cm	maa	ama	CTC.		CTC	ጥጥጥ	GCG	тст		719
GGG	GTG	GTG	ACA	AGT	GTG	ATC	ACT	TGG	GIG	GIG	אן א	Val	Dhe	Δla	Ser		,
Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	vai	val	MIG	vai	rnc	71.20	160		
145					150		202	mam	<i>-</i>	155	מאא	CCT	Стт	СДТ			767
CTC	CCA	GGA	ATC	ATC	TTT	ACC	AGA	TCT	CAA	AAA	CAA	Clv	Len	Hie	Tyr		
Leu	Pro	Gly	Ile		Phe	Thr	Arg	Ser	GIN	ьуs	GIU	GIY	Пеп	175	- 7 -		
				165					170	C 3 M	» cm	ርአጥ	CTT		CCT		815
ACC	TGC	AGC	TCT	CAT	TTT	CCA	TAC	ATT.	AAA	GAT	AGI	UAI	LOU	Glv	Δla		013
Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	ile	ьуs	Asp	Ser	HIS	190	Gry	AIG		
			180					185			ama	000		CCT	א א א		863
GGT	CCT	GCC	GCT	GCT	TGT	CAT	GGT	CAT	CTG	CTA	CTC	03	WWI	DYO	Tyc		005
Gly	Pro	Ala	Ala	Ala	Cys	His	Gly	His	Leu	Leu	Leu	GIY	ASII	PIO	пур		
		195					200					205					914
AAC	TCT	GCT	TCG	GTG	TCG	AAA	TGA	GAAG.	AAG .	AGGC	ACAG	رين ل	1616	MUGC	T		917
Asn	Ser	Ala	Ser	Val	Ser	Lys											
	210					215								നനഗന	CCMMCA		974
TATCTTCACC ATCATGATTG TTTATTTTCT CTTCTGGGCT CCCTACAACA TTGTCCTTCT 9											714						

CCAAGCTATG CAGC	CAGGAAT TCTTTGGCC GTGACAG AGACTCTTG GGGGAGA AGTTCAGAA	G GATGACGCAC A CTACCTCTTA	TGCTGCATCA GTCTTCTTCC	ACCCCATCAT AAAAGCACAT	1034 1094 1154 1214
CTCACTTTAC ACC	TGCAAAT GCTGTTCTA CGATCCA CTGGGGAGC	A GGAAATATCT	GTGGGCTTGT	GACACGGACT	1274 1334
GCCTGGGGGT GGTT	GACCCAG TCAGAGTTG TGGGAGG TCTTTTTA TTGGCAT CTGTTTAAA	A AAGGAAGTTA	CTGTTATAGA	GGGTCTAAGA	1394 1442

#### (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 184 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- 닭ii) MOLECULE TYPE: protein
- xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr 10 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu 25 20 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn 40 Metileu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met 55 Thr‡Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu 75 70 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe 90 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 105 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 125 120 115 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 150

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165

Thr Cys Ser Ser His Phe Pro Tyr 180

### (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 352 amino acids
  - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu 25 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn 40 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met 55 . Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu 75 70 Leu_Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 105 100 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 125 120 115 Ala Wal Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 140 135 Gly Wal Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 150 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 170 165 Thracys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn 190 185 180 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu 205 200 Val'Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys 215 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile 235 230 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu 250 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser 265 260 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr 285 280 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe 300 295 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe 310 Cys Lys Cys Cys Ser Ile Phe Gln Glu Ala Pro Glu Arg Ala Ser 330 325 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu 345

#### (2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 215 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu 25 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn 40 Met Deu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met 55 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu 75 70 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe 90 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 105 100 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 120 115 Ala val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 140 **1**30 135 Gly 🖟 al Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 155 150 Leu⊨Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 170 165 Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala 190 185 Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Gly Asn Pro Lys 205 200 195 Asn Ser Ala Ser Val Ser Lys 215. 210

- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 360 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val 55 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr 75 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met 105 100 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile 125 120 Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His 140 135 Wal Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr 155 150 Ser Wal Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile 170 165 Ile phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro 190 185 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile 200 LeuŒly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly 220 215 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg 235 230 Alagval Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp 250 245 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe 265 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Ile Gln 285 280 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile 300 295 Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Ile Ser Val Phe Phe 310 Arg Lys His Ile Xaa Xaa Xaa Phe Cys Lys Gln Cys Pro Val Phe Tyr 330 325 Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly 350 345 Glu Gln Glu Val Ser Ala Gly Leu 360 355

#### (2) INFORMATION FOR SEQ ID NO:8:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	•	•	_												
				_					1()					10	Tyr.
			20				Cys	25					J 0		
		2 5	Phe				Leu 40					43			
	- 0	Gly				55	Val				60				
					70	Ile	Tyr			10					00
₩±±				95	Thr		Pro		90					) )	
<del></del>			100	Phe			Gly	105					110		
-115		115	Gly				Glu 120	Ile				145			
IJĒ	120	Arg				175	Val				140				
Arg	Thr				150	Val	Ile			155					100
FR E				165	Leu		Glu		170					1, ,	
			100	Thr			Ser	185					100		
		- A C	Arg				Thr 200	Ile				200			
	~ ~ ~	Pro				ソート	Ala				220				
225					つての	Xaa				233				•	Leu 240
	Phe			215	Ala				250					200	Asn
			260	Ile	Ser			ンんち	Ser	Leu			2/0		Asn
		275	Ser	Lys			Asp 280	Leu				203			
	200	Tyr	Ser			295	Met	Asn			300				
205		Arg			310	Tyr	Ile			212	Phe	His			
	Met			225	Arg	Tyr	Ile		- 3.3 U	Leu	Pro			222	
Glu	Arg	Ile		Ser	Val	Ser	Pro	Ser 345	Thr	Ala	Glu	Pro	Glu 350	Ile	Ser
Ile	Val	Phe	340												

355

### (2) INFORMATION FOR SEQ ID NO:9:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: None

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

-				_	Thr				IU						
2_3			20		Thr			25					J 0		
<b>\$1.5</b>		2 -	Leu		Pro		<b>A</b> ()					ェン			
111	EΛ	Gly			Leu	55					00			~	
~ <del>-      </del>	Lys				Ser 70					75					00
Lew				95	Thr				90					75	
Asp M			100		Gly			105					TTO		
Tyr		115			Tyr		120					123			
	120				Ala	735					740				
1 4 5					Gly 150					TOO					<b>±</b> 00
				165	Met				170					1,5	-
			100		Thr			185					100		
		105			Phe		7110					200			
	212				Val	シーち					220				
つつに					Pro 230					233					
				215					250					233	Asn
			$\gamma \in \Omega$					- 255					2,0		Glu
		つつに					- 280					200			Val
Ile	Ala 290	Tyr	Thr	His	Cys	Cys 295	Val	Asn	Glu	val	300	ıyı	wra	FILE	Val

Gly Glu Arg Phe Arg Lys Tyr Ile Arg Gln Leu Glu His Arg Arg Val 305 310 315 320

Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Ile 325 330 335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Ile Ser 340

Ala Gly Phe 355

#### (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 360 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

W Mee Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr 10 Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu 20 G⊫y Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu 40 Va Glu Val Phe Gly Leu Ile Gly Asn Ser Val Val Val Leu Val Leu 60 55 Phe Lys Tyr Lys Arg Ile Arg Ser Met Thr Asp Val Tyr Leu Leu Asn 75 Lew Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly 85 Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Ile Cys Lys Met 110 105 100 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val ---125 120 115 Met Ile Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Glu 140 135 Xaa Xaa Xaa Ala Arg Thr Ile Ile Tyr Gly Val Ile Thr Ser Leu Ala 155 150 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Ile Phe Ser 170 165 Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser 190 185 Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile 200 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met 215 210 Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala 235 230 Val Lys Met Ile Phe Ala Val Val Leu Phe Leu Gly Phe Trp Thr

250 245 Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val 265 260 Ile Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala 280 275 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr 300 295 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Ile Gln Leu Phe Lys 315 310 Xaa Xaa Xaa Gly Leu Phe Val Ile Cys Gln Tyr Cys Gly Leu Leu Gln 330 325 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met 345 Asp His Asp Leu His Asp Ala Leu 355

#### (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 amino acids
  - (B) TYPE: amino acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

The Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn 15 10 15 15

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu 20 25 30

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys 35 40 45

Arg Asn Glu Lys Lys Arg 50

#### (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 147 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTCCATACA GTCAGTATCA ATTCTGGAAG AATTTCCAGA CATTAAAGAT AGTCATCTTG

GGGCTGGTCC TGCCGCTGCT TGTCATGGTC ATCTGCTACT CGGGAATCCT AAAAACTCTG

120

CTTCGGTGTC GAAATGAGAA GAAGAGG

	(2) INFORMATION FOR SEQ ID NO:13:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 34 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
_	Pro Tyr Ile Lys Asp Ser His Leu Gly Ala Gly Pro Ala Ala Ala 10	
1 Cys	His Gly His Leu Leu Gly Asn Pro Lys Asn Ser Ala Ser Val 20 25 30	
Ser	Lys	
o u u n	(2) INFORMATION FOR SEQ ID NO:14:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 27 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	
I II IC	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO.14.	27
O	(2) INFORMATION FOR SEQ ID NO:15:	
•	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 27 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
:	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
CTG	GATCTAGA GCCATGTGCA CAACTCT	2
	(2) INFORMATION FOR SEQ ID NO:16:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

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	(xi)\SEQUENCE DESCRIPTION: SEQ ID NO:16:	•	
CCTGG	CTGTC GTCCATGCTG	·	20
	(2) INFORMATION FOR SEQ ID NO:17:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 27 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	1	
ርጥር እጥ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:		2
	CIAGA GCCITOTO		